

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2004, 10:04:27 ; Search time 828.719 Seconds

(without alignments)
1569.037 Million cell updates/sec

Title: US-09-986-381-1

Perfect score: 30
Sequence: 1 gccgctccagctgcttactcttact 30Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBank.*

1: gb_da.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
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9: gb_pr.*
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11: gb_ats.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_da.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_ats.*
28: em_un.*
29: em_vl.*
30: em_hgt_hum.*
31: em_hgt_inv.*
32: em_hgt_other.*
33: em_hgt_mus.*
34: em_hgt_pln.*
35: em_hgt_rod.*
36: em_hgt_mam.*
37: em_hgt_vrt.*
38: em_sy.*
39: em_hgt_hum.*
40: em_hgt_mus.*
41: em_hgt_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	799	9 HSP5314	X92659 H.sapiens 1
2	30	100.0	3407	9 HSP5314	AF136270 Homo sapi
3	30	100.0	3423	9 HSP5314	AF151520 Homo sapi
4	30	100.0	121017	9 HSP5314	AC087388 Homo sapi
5	30	100.0	166941	2 AC008049	AC008049 Homo sapi
6	28.4	94.7	600	6 192482	192482 Sequence 2
7	28.4	94.7	4360	9 AB018045	AB018045 Homo sapi
8	28.4	94.7	20303	9 HSP5314	X54156 Human p53 g
9	28.4	94.7	20303	9 HSP5314	U94768 Human p53 g
10	25.2	84.0	163542	2 AC129071	AC129071 Pan trogl
11	25.2	84.0	174521	2 AC127468	AC127468 Papio anu
12	25.2	84.0	176927	2 AC127469	AC127469 Papio anu
13	25.2	84.0	218485	2 AC127470	AC127470 Pan trogl
14	22.8	76.0	170162	10 AL807748	AL807748 Mouse DNA
15	22.2	74.0	201076	2 AC119349	AC119349 Rattus no
16	22.2	74.0	241561	2 AC098420	AC098420 Rattus no
17	22	73.3	22	6 AX037125	AX037125 Sequence
18	22	73.3	945	10 AY073823	AY073823 Mus muscu
19	22	73.3	945	10 AY17467	AY17467 Mus muscu
20	22	73.3	262405	2 AC102976	AC102976 Rattus no
21	21.8	72.7	273729	2 AC106147	AC106147 Rattus no
22	21.6	72.0	4718	4 AY152693	AY152693 Bos tauru
23	21.6	72.0	200535	10 AL671880	AL671880 Mouse DNA
24	21.6	72.0	216123	2 AC036146	AC036146 Mus muscu
25	21.6	72.0	221117	2 AC023174	AC023174 Mus muscu
26	21.2	70.7	2068	9 HSM805269	AL834243 Homo sapi
27	21.2	70.7	2284	6 AX713711	AX713711 Sequence
28	21.2	70.7	2284	6 AK055435	AK055435 Homo sapi
29	21.2	70.7	4373	9 AB046781	AB046781 Homo sapi
30	21.2	70.7	4428	9 AF322916	AF322916 Homo sapi
31	21.2	70.7	4429	4 AF322915	AF322915 Bos tauru
32	21.2	70.7	19795	9 HSTGCMDE	X57331 Human immu
33	21.2	70.7	83775	2 AC022466	AC022466 Homo sapi
34	21.2	70.7	149287	9 AC087699	AC087699 Homo sapi
35	21.2	70.7	151567	2 AC145503	AC145503 Canis fam
36	21.2	70.7	154160	2 AC046154	AC046154 Homo sapi
37	21.2	70.7	155760	2 AC010076	AC010076 Homo sapi
38	21.2	70.7	167208	2 AC034190	AC034190 Homo sapi
39	21.2	70.7	169802	9 CNGS01DR2	AL122127 Human chr
40	21.2	70.7	173534	9 AC007920	AC007920 Homo sapi
41	21.2	70.7	199277	2 AC145445	AC145445 Canis fam
42	21.2	70.7	207841	2 AC072019	AC072019 Homo sapi
43	21	70.0	89936	8 AP004532	AP004532 Locust cor
44	21	70.0	155372	2 AC108818	AC108818 Mus muscu
45	21	70.0	163396	9 AL161445	AL161445 Human DNA

ALIGNMENTS

RESULT 1
HSP5314
LOCUS HSP5314 799 bp DNA linear PRI 25-NOV-1996
DEFINITION H.sapiens intron 4 from p53 gene.
ACCESSION X92659
VERSION X92659.1 GI:1177472
KEYWORDS p53 gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Shamsheer M. and Montano X.
TITLE Analysis of intron 4 of the p53 gene in human cutaneous melanoma
JOURNAL Gene 176 (1-2), 259-262 (1996)

MEDLINE 97075940
 PUBMED 8918263
 REFERENCE 2 (bases 1 to 799)
 AUTHORS Montano, X.C.
 TITLE Direct Submission
 JOURNAL Submitted (29-OCT-1995) X.C. Montano, Imperial Cancer Research Fund, Viral Mediated Cell Differentiation Lab, PO Box 123, Lincoln's Inn Fields, LONDON, WC2A 3PX, UK

FEATURES
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 /cell_type="melanoma"
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 /number=4
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 /gene="p53"
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 /number=5

exon
 intron
 exon

ORIGIN

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 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGCTCCAGTTCCTTATCTGTTCACT 30
 Db 707 GCCGCTCCAGTTCCTTATCTGTTCACT 736

RESULT 2
 LOCUS HOMOTSPI 3407 bp DNA linear PRI 28-MAR-2002
 DEFINITION Homo sapiens tumor suppressor protein p53 (P53) gene, exons 2
 through 9.
 ACCESSION AF136270
 VERSION AF136270.1 GI:4732144
 KEYWORDS
 SEGMENT
 SOURCE
 ORGANISM
 Homo sapiens (human)
 1 of 2
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 3407)
 Anderson, C.W. and Allalunis-Turner, M.J.
 Human TP53 from the malignant glioma-derived cell lines M059J and M059K has a cancer-associated mutation in exon 8
 Radiat. Res. 154 (4), 473-476 (2000)
 11023613
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Bell Avenue, Upton, NY 11973-5000, USA

FEATURES
 source 1..3407
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 /mol_type="genomic DNA"
 /db_xref="ATCC:CCL-185"
 /db_xref="taxon:9606"
 /cell_line="A549"
 /note="A549 cells express wild-type p53 protein"
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exon
 exon
 exon
 exon
 exon
 exon
 exon
 exon
 exon
 exon

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGCTCCAGTTCCTTATCTGTTCACT 30
 Db 1483 GCCGCTCCAGTTCCTTATCTGTTCACT 1512

RESULT 3
 LOCUS HSM059JPI 3423 bp DNA linear PRI 28-MAR-2002
 DEFINITION Homo sapiens tumor suppressor protein p53 (P53) gene, exons 2
 through 9.
 ACCESSION AF135120
 VERSION AF135120.1 GI:4731629
 KEYWORDS
 SEGMENT
 SOURCE
 ORGANISM
 Homo sapiens (human)
 1 of 2
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 3423)
 Mirzayans, R.
 Isolation of two cell lines from a human malignant glioma specimen differing in sensitivity to radiation and chemotherapeutic drugs
 Radiat. Res. 134 (3), 349-354 (1993)
 93303270
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Bell Avenue, Upton, NY 11973-5000, USA

FEATURES
 source 1..3423
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /cell_type="M059J"

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2004, 10:04:27 ; Search time 911.591 Seconds

(without alignments)
1569.037 Million cell updates/sec

Title: US-09-986-381-3

Perfect score: 33
Sequence: 1 gccaagtagcatcgtatccagcgcaagtcagatag 33

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenBank: 1: gb_ba: 2: gb_hcg: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pac: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_ba: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pat: 24: em_ph: 25: em_pi: 26: em_ro: 27: em_sts: 28: em_un: 29: em_vl: 30: em_hcg_hum: 31: em_hcg_inv: 32: em_hcg_other: 33: em_hcg_mus: 34: em_hcg_pln: 35: em_hcg_rtd: 36: em_hcg_mam: 37: em_hcg_vit: 38: em_sy: 39: em_hugo_hum: 40: em_hugo_mus: 41: em_hugo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	33	100.0	133	9	S81486
C 2	33	100.0	160	9	S66666 p53 {altern
C 3	33	100.0	4360	9	AB018045 Homo sapi
C 4	33	100.0	20303	9	HSP536
C 5	33	100.0	20303	9	HSU94788
C 6	33	100.0	121017	9	AC087388 Homo sapi
C 7	33	100.0	163542	2	AC129071 Pan trogl
C 8	33	100.0	166941	2	AC008049 Homo sapi
C 9	33	100.0	174521	2	AC127468
C 10	33	100.0	176827	2	AC127469
C 11	33	100.0	218485	2	AC127470
C 12	24	72.7	199541	2	BX530058 Danio rer
C 13	23	69.7	118985	2	AC087152 Mus muscu
C 14	23	69.7	173547	2	AC116828
C 15	22.2	67.3	24142	6	BX537050 Sequence
C 16	22.2	67.3	168876	2	AC126535
C 17	22.2	67.3	233233	2	AC094145
C 18	22.2	67.3	236933	2	AC111937
C 19	22.2	67.3	300312	2	AC111822
C 20	22.2	67.3	335551	2	AC115496
C 21	22	66.7	112904	9	AC027342
C 22	22	66.7	159524	9	CNS01DUO
C 23	22	66.7	184536	2	AC068682
C 24	22	66.7	210385	10	AC106128
C 25	21.8	66.1	102743	9	AL645507 Human DNA
C 26	21.8	66.1	145111	2	AL390245
C 27	21.6	65.5	205811	2	AC113095
C 28	21.4	64.8	490	11	GI0379
C 29	21.4	64.8	74982	9	AC067958
C 30	21.4	64.8	109337	2	AC139114
C 31	21.4	64.8	152533	9	AC008483
C 32	21.4	64.8	152895	2	AC031979
C 33	21.4	64.8	154333	5	BX005316 Zebrafish
C 34	21.4	64.8	169328	2	AC016281
C 35	21.4	64.8	169714	2	AC116843
C 36	21.4	64.8	170817	9	AL513166 Human DNA
C 37	21.4	64.8	183787	9	AC010423 Homo sapi
C 38	21.4	64.8	202433	2	AC121504 Mus muscu
C 39	21	63.6	36521	2	AC020203
C 40	21	63.6	67297	3	AC005135
C 41	21	63.6	173188	3	AC093196
C 42	21	63.6	198667	10	AC111144
C 43	21	63.6	265099	3	AB003626 Drosophil
C 44	20.8	63.0	95983	9	AC004874
C 45	20.8	63.0	100785	2	AC069169 Homo sapi

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
S81486/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					

et.al.
Hereditary and acquired p53 gene mutations in childhood acute lymphoblastic leukemia
J. Clin. Invest. 89 (2), 640-647 (1992)

JOURNAL
MEDLINE
1737852
PUBMED
Genbank staff at the National Library of Medicine created this entry [NCBI gisbseq 81486] from the original journal article.
This sequence comes from Figure 2.
Map location: chromosome 17 band p13.1.
133 bp insertion intron 9.
Location/Qualifiers
1. .133
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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COMMENT
FEATURES
source

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 GTCAAGTACATCTGTATCAGGCAAGTCATAG 33
85 GTCAAGTACATCTGTATCAGGCAAGTCATAG 53

RESULT 2
S6666/c
LOCUS
DEFINITION
p53=tumor suppressor [alternatively spliced, exon 9-10] [human, Molt-4, T-lymphoblastic leukemia cell line, mRNA partial], 160 nt.
S66666
S66666.1 GI:436292

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 160)
Chow, V.T., Quek, H.H. and Tock, E.P.
Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphoblastic leukemia cell line
Cancer Lett. 73 (2-3), 141-148 (1993)
94036762
JOURNAL
MEDLINE
8221626
PUBMED
Genbank staff at the National Library of Medicine created this entry [NCBI gisbseq 139316] from the original journal article.
This sequence comes from Fig. 2.
Map location: 17.
Location/Qualifiers
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1. .160
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1. .48
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/note="tumor suppressor; This sequence comes from Fig. 2"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
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RESULT 3
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LOCUS
DEFINITION
Homo sapiens HSP70-1 gene for heat shock protein 72, spliced variant, partial cds.
AB018045
AB018045.1 GI:4691417
HSP70-1; heat shock protein 72; HSP70-Hom; alternative splicing.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (sites)
Shimizu, S., Nomura, K., Ujihara, M. and Demura, H.
An additional exon of stress-inducible heat shock protein 70 gene (HSP70-1)
Biochem. Biophys. Res. Commun. 257 (1), 193-198 (1999)
99194576
MEDLINE
10092532
2 (bases 1 to 4360)
Nomura, K. and Shimizu, S.
Direct Submission
Submitted (27-SEP-1998) Kaoru Nomura, Tokyo Women's Medical University, Department of Medicine 2; 8-1 Kawadacho, Shinjuku-ku, Tokyo 162-8666, Japan (E-mail: nomura7@parkcity.ne.jp, Tel:81-3-3353-8111 (ex.39223), Fax:81-3-3357-6475)
Sequence updated (26-Oct-1998).
Location/Qualifiers
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/mol_type="genomic DNA"
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transcription usually starts from exon 2"
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